STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

EFS

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/552,324A_

Source: _1FWO_

Date Processed by STIC: _3/6/07_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
>   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
<u>Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:</u>

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , **EFS Submission User Manual - ePAVE)**
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: *10/552, 324A*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
    Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
    prevent "wrapping."

2____Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
    Numbering use space characters, instead.

4____Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
    ensure your subsequent submission is saved in ASCII text.

5____Variable Length Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
    each n or Xaa can only represent a single residue. Please present the maximum number of each
    residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
    "bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the
    previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
    the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
    Artificial or Unknown sequences.

7____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
    (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    This sequence is intentionally skipped
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
    (NEW RULES) <210> sequence id number
    <400> sequence id number
    000

9____Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
    (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
    Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
    is Artificial Sequence. (see item 11 below)

11____Use of <220> Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use
    of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
    Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
    explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
    Sequence Rules

12____PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
    "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
    listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

IFWO

RAW SEQUENCE LISTING   DATE: 03/06/2007
PATENT APPLICATION: US/10/552,324A   TIME: 11:16:32

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Output Set: N:\CRF4\03062007\J552324A.raw

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        3 <110> APPLICANT: Igeneon Krebs-Immuntherapie Forschungs- & Entwickl
        5 <120> TITLE OF INVENTION: Immunogenic Recombinant Antibody
        7 <130> FILE REFERENCE: Immunogenic Recombinant AB
C-->    9 <140> CURRENT APPLICATION NUMBER: US/10/552,324A
C-->   10 <141> CURRENT FILING DATE: 2005-10-07
       12 <160> NUMBER OF SEQ ID NOS: 5
       14 <170> SOFTWARE: PatentIn Ver. 2.1
       16 <210> SEQ ID NO: 1
       17 <211> LENGTH: 3973
       18 <212> TYPE: DNA
       19 <213> ORGANISM: Artificial Sequence
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       27 atgacccaat ctcccaaatc catgtccatg tcagtaggag agagggtcac cttgacctgc 180
W-->   28 aaggccagtg agaatgtggt tacttatgtt tcttggtatc aacagaaacc agagcagtct 240
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       30 ggcagtggat ctgcaacaga tttcactctg accatcagca gtgtgcaggc tgaagacctt 360
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56 cctgagccag tgaccttgac ctggaactct ggatccctgt ccagtggtgt gcacaccttc 1920
57 ccagctgtcc tgcagtctga cctctacacc ctcagcagct cagtgactgt aacctcgagc 1980
58 acctggccca gccagtccat cacctgcaat gtggcccacc cggcaagcag caccaaggtg 2040
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95 <212> TYPE: PRT
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99 <223> OTHER INFORMATION: Description of Artificial Sequence mAB 17-1A
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106              20                  25                  30
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give source

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108 Pro Gly Thr Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe
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111 Thr Asn Tyr Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
112      50              55                  60
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115  65                  70                  75                  80
117 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
118              85                  90                  95
120 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
121          100                 105                 110
123 Tyr Phe Cys Ala Arg Asp Gly Pro Trp Phe Ala Tyr Trp Gly Gln Gly
124          115                 120                 125
126 Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Ala Pro Ser Val Tyr
127      130                 135                 140
129 Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu
130 145                 150                 155                 160
132 Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp
133              165                 170                 175
135 Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
136          180                 185                 190
138 Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser
139          195                 200                 205
141 Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser
142      210                 215                 220
144 Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys
145 225                 230                 235                 240
147 Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro
148              245                 250                 255
150 Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser
151              260                 265                 270
153 Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp
154          275                 280                 285
156 Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr
157 290                 295                 300
159 Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val
160 305                 310                 315                 320
162 Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu
163          325                 330                 335
165 Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg
166          340                 345                 350
168 Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val
169          355                 360                 365
171 Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr
172     370                 375                 380
174 Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr
175 385                 390                 395                 400
177 Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu
178              405                 410                 415
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181              420                   425                   430
183 Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu
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187     450                   455                   460
189 Lys
190 465
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194 <211> LENGTH: 243
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Description of Artificial Sequence mAB 17-1A
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206            20                   25         .          30
208 Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly Glu Arg Val
209          35                   40                   45
211 Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp
212     50                   55                   60
214 Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala
215   65         .          70                   75                  80
217 Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
218            85         .          90                   95 ·
220 Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
221         .100                  105                  110
223 Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly
224     115                  120                  125
226 Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val
227     130                  135                  140
229 Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser
230 145                  150                  155                  160
232 Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys
233            165                  170 ·                 175
235 Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp
236            180                  185                  190
238 Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu
239     195                  200                  205
241 Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu
242     210                  215                  220
244 Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg
245 225                  230                  235                  240
247 Asn Glu Cys
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252 <211> LENGTH: 243
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254 <213> ORGANISM: Artificial Sequence
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264             20                  25                  30
266 Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly Glu Arg Val
267         35                  40                  45
269 Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp
270      50                  55                  60
272 Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala
273  65                  70                  75                  80
275 Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
276              85                  90                  95.
278 Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
279          100                 105                 110
281 Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly
282      115                 120                 125
284 Gly Gly Thr Lys Leu Glu Ile Arg Arg Ala Asp Ala Ala Pro Thr Val
285      130                 135                 140
287 Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser
288 145                 150                 155                 160
290 Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys
291              165                 170                 175
293 Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp
294          180                 185                 190
296 Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu
297          195                 200                 205
299 Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu
300      210                 215                 220
302 Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg
303 225                 230                 235                 240
305 Asn Glu Cys
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310 <211> LENGTH: 243
311 <212> TYPE: PRT
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Description of Artificial Sequence mAB 17-1A
317 <400> SEQUENCE: 5
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319  1               5                   10                  15
321 Phe Ile Ser Ile Leu Leu Trp Leu Tyr Gly Ala Asp Gly Asn Ile Val
322             20                  25                  30
324 Met Thr Gln Ser Pro Arg Ser Met Ser Met Ser Val Gly Glu Arg Val
325         35                  40                  45
327 Thr Leu Thr Cys Arg Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp
328      50                  55                  60
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/06/2007
PATENT APPLICATION: US/10/552,324A   TIME: 11:16:33

Input Set : N:\efs\03_06_07\10552324A_efs\4518-0111PUS1-ST25.txt
Output Set: N:\CRF4\03062007\J552324A.raw

erra Explanation

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 213,288

FYI

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:5; Line(s) 368,369,370,371,372,373,374,375,376,377,378,379,380,381,382

VERIFICATION SUMMARY   DATE: 03/06/2007
PATENT APPLICATION: US/10/552,324A   TIME: 11:16:33

Input Set : N:\efs\03_06_07\10552324A_efs\4518-0111PUS1-ST25.txt
Output Set: N:\CRF4\03062007\J552324A.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:1
L:28 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:1
L:28 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:180
M:341 Repeated in SeqNo=1